

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 16, 2005, 16:12:05 ; Search time 69.2267 Seconds
(without alignments)
2810.909 Million cell updates/sec

Title: US-10-003-356-5
Perfect score: 1986
Sequence: 1 LPHSVCTDVCPPTGTRGFVQ.....TVSTVLDDRVLVYMCPLKIQ 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1906	96.0	755	2 Q8NGV9	Q8ngv9 homo sapien
2	1749	88.1	365	2 Q8TDU1	Q8tdul homo sapien
3	1450	73.0	428	2 O70413	O70413 rattus norv
4	1444	72.7	912	2 O70410	O70410 mus musculu
5	904.5	45.5	230	2 O70414	O70414 rattus norv
6	791.5	39.9	458	2 O93555	O93555 carassius a
7	787.5	39.7	848	2 O93553	O93553 carassius a
8	775.5	39.0	362	2 Q9PSY1	Q9psyl carassius a
9	775.5	39.0	408	2 O93558	O93558 carassius a
10	769.5	38.7	844	2 O93552	O93552 carassius a
11	755.5	38.0	350	2 O93556	O93556 carassius a
12	753.5	37.9	880	2 O73639	O73639 fugu rubrip
13	751	37.8	875	2 O73640	O73640 fugu rubrip
14	747	37.6	856	2 O73638	O73638 fugu rubrip
15	736.5	37.1	1027	2 Q8JI04	Q8ji04 squalus aca
16	722	36.4	864	2 O73637	O73637 fugu rubrip
17	715.5	36.0	783	2 Q8CDP3	Q8cdp3 mus musculu
18	714.5	36.0	1079	1 CASR_MOUSE	Q9qy96 mus musculu
19	714.5	36.0	1079	1 CASR_RAT	P48442 rattus norv
20	713.5	35.9	1079	2 Q80ZA8	Q80za8 rattus norv
21	711.5	35.8	1078	1 CASR_HUMAN	P41180 homo sapien
22	709.5	35.7	1085	1 CASR_BOVIN	P35384 bos taurus
23	702.5	35.4	868	2 O73636	O73636 fugu rubrip
24	696.5	35.1	854	2 Q6UNX3	Q6unx3 ictalurus p
25	696	35.0	941	2 Q6XAF1	Q6xaf1 salmo salar
26	696	35.0	941	2 Q6XAF3	Q6xaf3 salmo salar
27	678.5	34.2	940	2 O73635	O73635 fugu rubrip
28	675	34.0	940	2 Q90WL6	Q90wl6 sparus aura
29	660	33.2	850	2 Q6XAF2	Q6xaf2 salmo salar
30	644	32.4	157	2 Q99PC0	Q99pc0 rattus norv
31	640.5	32.3	866	2 O35268	O35268 rattus norv

32	639.5	32.2	855	2 O70409	O70409 mus musculu
33	638.5	32.2	855	2 Q6TAC4	Q6tac4 mus musculu
34	636.5	32.0	845	2 Q80Z08	Q80z08 mus musculu
35	621.5	31.3	695	2 O35272	O35272 rattus norv
36	620.5	31.2	339	2 O70411	O70411 rattus norv
37	614.5	30.9	501	2 Q86UN7	Q86un7 homo sapien
38	612.5	30.8	852	2 O35192	O35192 mus musculu
39	607.5	30.6	865	2 Q80Z09	Q80z09 mus musculu
40	606.5	30.5	667	2 O35267	O35267 rattus norv
41	605.5	30.5	723	2 O35193	O35193 mus musculu
42	605.5	30.5	779	2 O35269	O35269 rattus norv
43	603.5	30.4	803	2 O35191	O35191 mus musculu
44	600.5	30.2	768	2 O35266	O35266 rattus norv
45	598.5	30.1	850	2 O35189	O35189 mus musculu

ALIGNMENTS

RESULT 1

Q8NGV9					
ID	Q8NGV9	PRELIMINARY;	PRT;	755 AA.	
AC	Q8NGV9;				
DT	01-OCT-2002 (TrEMBLrel. 22, Created)				
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	Seven transmembrane helix receptor.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,				
RA	Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;				
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AB065664; BAC05890.1; --				
DR	GO; GO:0016021; C:integral to membrane; IEA.				
DR	GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.				
DR	GO; GO:0004872; F:receptor activity; IEA.				
DR	InterPro; IPR001828; ANF_receptor.				
DR	InterPro; IPR000337; GPCR_Mgr.				
DR	Pfam; PF00003; 7tm 3; 1.				
DR	Pfam; PF01094; ANF_receptor; 1.				
DR	PRINTS; PR00248; GPCRMR.				
DR	PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.				
KW	Receptor; Transmembrane.				
SQ	SEQUENCE 755 AA; 83791 MW; 04D56AD8917BDA1F CRC64;				

Query Match 96.0%; Score 1906; DB 2; Length 755;
Best Local Similarity 99.7%; Pred. No. 1.5e-130;
Matches 367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	13	GTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQC	GEDYWSNAQKSECVLKEVEYLAY	72
Db	388	GLGRGFVQREPICCFDSIPCADGHVSRKPGERECEQC	GEDYWSNAQKSECVLKEVEYLAY	447
QY	73	DEALGFTLVLSVFGAFVLA	VTAVYVTHRHTPLVNASDWQLGFLIQVSLIIMLLSSMLF	132
Db	448	DEALGFTLVLSVFGAFVLA	VTAVYVTHRHTPLVNASDWQLGFLIQVSLIIMLLSSMLF	507
QY	133	IDKPHNWSMAGQVTIALGFSLCLSLCKTSSSLFLAYRISK	SKTQLTSMHPLYRKIIIVL	192
Db	508	IDKPHNWSMAGQVTIALGFSLCLSLCKTSSSLFLAYRISK	SKTQLTSMHPLYRKIIIVL	567
QY	193	ISVLAIEIGICTAYLILEP	PMVKNMESQNTKIILGCNEISIEFLYSNMGIDAPLALLCFL	252
Db	568	ISVLAIEIGICTAYLILEP	PMVKNMESQNTKIILGCNEISIEFLYSNMGIDAPLALLCFL	627
QY	253	TTFVARQLPDNYEGKCITF	GMVFFIIWMSFVPVYLSTKGKFKMAVEIFAILASSHGLL	312
Db	628	TTFVARQLPDNYEGKCITF	GMVFFIIWMSFVPVYLSTKGKFKMAVEIFAILASSHGLL	687

QY 313 GCIFAPKCLIIILLRPERNTSEIVCGRVSTTDNCIQLTSAFVSSELNNTTSTVLDLDRVLI 372
Db 688 GCIFAPKCLIIILLRPERNTSEIVCGRVSTTDNCIQLTSAFVSSELNNTTSTVLDLDRVLI 747
QY 373 YMCPLKLIQ 380
Db 748 YMCPLKLIQ 755

RESULT 2

Q8TDU1 ID Q8TDU1 PRELIMINARY; PRT; 365 AA.
AC Q8TDU1;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Putative G-protein coupled receptor.
GN Name=GPCR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takasasu H., Mitaku S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083610; BAB89323.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.

SQ SEQUENCE 365 AA; 40920 MW; 9BFC4F8EFA873133 CRC64;

Query Match 88.1%; Score 1749; DB 2; Length 365;
Best Local Similarity 99.1%; Pred. No. 2e-119;
Matches 341; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 37 VSRKPGERECEQCGDYWSNAQSECVLKEVEYLAYDEALGFTLVLSVFGAFVVLAVTA 96
Db 22 VLRSIGERECEQCGDYWSNAQSECVLKEVEYLAYDEALGFTLVLSVFGAFVVLAVTA 81
QY 97 VYVHRHTPLVNASDWQLGFLIQVSLIIMLLSSMLFIDKPHNWSWAGQVTLALGFSCL 156
Db 82 VYVHRHTPLVNASDWQLGFLIQVSLIIMLLSSMLFIDKPHNWSWAGQVTLALGFSCL 141
QY 157 SCLLGTSSFLAYRISKSTQLTSMHPLYRKIIIVLSVLAIEIGICTAYLILEPPMVYKN 216
Db 142 SCLLGTSSFLAYRISKSTQLTSMHPLYRKIIIVLSVLAIEIGICTAYLILEPPMVYKN 201
QY 217 MESQNTKIILGCNEISIEFLYSMFGIDAFLLALCFLTTFVARQLPDNYVEGKCITFGMLV 276
Db 202 MESQNTKIILGCNEISIEFLYSMFGIDAFLLALCFLTTFVARQLPDNYVEGKCITFGMLV 261
QY 277 FFIWMSFVPVYLSKGFKMAVEIFAILASSHGLLGICIFAPKCLIIILLRPERNTSEIVC 336
Db 262 FFIWMSFVPVYLSKGFKMAVEIFAILASSHGLLGICIFAPKCLIIILLRPERNTSEIVC 321
QY 337 GRVSTTDNCIQLTSAFVSSELNNTTSTVLDLDRVLIYMCPLKQ 380
Db 322 GRVSTTDNCIQLTSAFVSSELNNTTSTVLDLDRVLIYMCPLKQ 365

RESULT 3

O70413 ID O70413 PRELIMINARY; PRT; 428 AA.
AC O70413;
DT 01-AUG-1998 (TremBLrel. 07, Created)
DT 01-AUG-1998 (TremBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)

DE Putative pheromone receptor V2R2 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vomeronasal neurons;
RX MEDLINE=97436753; PubMed=9292726; DOI=10.1016/S0896-6273(00)80946-0;
RA Ryba N.J., Tirindelli R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053989; AAC08416.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
FT NON TER 1 1
SQ SEQUENCE 428 AA; 47708 MW; BFB69A78F750E202 CRC64;

Query Match 73.0%; Score 1450; DB 2; Length 428;
Best Local Similarity 75.5%; Pred. No. 1.4e-97;
Matches 277; Conservative 35; Mismatches 55; Indels 0; Gaps 0;

QY 2 PHSVCTDVCPPGTGRGVQREPICCFDSSIPCADGHVSRKPGERECEQCGDYWSNAQSK 61
Db 62 PDSFCTQVCPGTRKGIROGQPICCFDSSIPCADGHVSRKPGERECEQCGDYWSNAQSK 121
QY 62 CVLKEVEYLAYDEALGFTLVLSVFGAFVVLAVTAVYVHRHTPLVNASDWQLGFLIQVS 121
Db 122 CVPKLVEFLAYEEALGFTLVLSVFGAFVVLAVTAVYVHRHTPLVNASDWQLGFLIQVS 181
QY 122 LIIMLLSSMLFIDKPHNWSWAGQVTLALGFSCLLGTSSFLAYRISKSTQLTLS 181
Db 182 LVITVLSMLFIDKPHNWSWAGQVTLALGFSCLLGTSSFLAYRISKSTQLTLS 241
QY 182 MHPLYRKIIIVLSVLAIEIGICTAYLILEPPMVYKNMESQNTKIILGCNEISIEFLYSMFG 241
Db 242 MSPYRKLIIVLCVGEIGVCAAYLVLEPPRMFKNIQPNVKIIFECNEGSIEFLCAIFG 301
QY 242 IDAFLLALCFLTTFVARQLPDNYVEGKCITFGMLVFFIWMSPVYVLSKGFKMAVEI 301
Db 302 FDVFLALLCFLTTFVARQLPDNYVEGKCITFGMLVFFIWMSPVYVLSKGFKMAVEI 361
QY 302 FAILASSHGLLGICIFAPKCLIIILLRPERNTSEIVCGRVSTTDNCIQLTSAFVSSELNNTT 361
Db 362 FAILASSYGLLGICIFLPKCFILLRPRKNTDETGVGRVPTVDRSIQLTSASVSSELNNTA 421
QY 362 VSTVLDL 368
Db 422 VSTVLDL 428

RESULT 4

O70410 ID O70410 PRELIMINARY; PRT; 912 AA.
AC O70410;
DT 01-AUG-1998 (TremBLrel. 07, Created)
DT 01-AUG-1998 (TremBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Putative pheromone receptor V2R2.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vomeronasal neurons;
RX MEDLINE=97436753; PubMed=9292726; DOI=10.1016/S0896-6273(00)80946-0;
RA Ryba N.J., Tirindelli R.;
RT "A new multigene family of putative pheromone receptors.";
RL Neuron 19:371-379(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Vomeronasal neurons;
RA Ryba N.J.P., Tirindelli R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053986; AAC08413.1; --
DR HSSP; P23385; 1EWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 912 AA; 102348 MW; 2C54FAB6DFBFA48D CRC64;

Query Match 72.7%; Score 1444; DB 2; Length 912;
Best Local Similarity 74.7%; Pred. No. 8e-97;
Matches 274; Conservative 37; Mismatches 56; Indels 0; Gaps 0;

QY 2 PHSVCTDVCPPGTRGFVQREPICCFDSIPCADGHVSRKPGERECEOCGEDYWSNAQKSE 61
Db 546 PDSFCTQVCPGTRKGIROGQIPCCFDCIPCADGYVSEKSGQRECDPCGEDDWSNAGSK 605

QY 62 CVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVYVHRHTPLVNASDWQLGLIQVS 121
Db 606 CVPKLVFLAYGEALGFTLVILSIFGALVVLAVTVVYVHRHTPLVKANDRELSFLIQMS 665

QY 122 LIIMLLSSMLFIDKPHNWSMAGQVTLALGFSLCLSGKTSSFLAYRISKSTQLTS 181
Db 666 LVITVLSLLFLGKPCNWSMARQITLALGFCLCLSSILGKTISLFFAYRISVSKTRLLS 725

QY 182 MHPLYRKIIIVLSVLAIEIGICTAYLILEPPMVYKNMESQNTKIILGCNEISIEFLYSMFG 241
Db 726 MHPIFRKLIIVLCVVGIGVCAAYLVLEPRMFKNIEIQNVKIIFECNEGSVEFLCSIFG 785

QY 242 IDAFLALLCFLTFVARQLPDNYYEGKCTIFGMLVFFIWMSPVYVLTSTGKFKMAVEI 301
Db 786 FDLVRLALLCFLTFVARQLPDNYYEGKCTIFGMLVFFIWMSPVYVLTSTGKFKMAVEI 845

QY 302 FAILASSHGLGCTFAPKCLIIILRPNTSEIVCGRVSTTDNCIQLTSAFVSSELNNTT 361
Db 846 FAILASSYGLLGLFLPKCFIILRPKRNTDETGVGRVPTVDRSIQLTSASVSSELNSTT 905

QY 362 VSTVLDD 368
Db 906 VSTVLDE 912

RESULT 5
O70414 PRELIMINARY; PRT; 230 AA.
ID O70414
AC O70414;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Putative pheromone receptor V2R2B (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vomeronasal neurons;
RX MEDLINE=97436753; PubMed=9292726; DOI=10.1016/S0896-6273(00)80946-0;
RA Ryba N.J., Tirindelli R.;
RT "A new multigene family of putative pheromone receptors.";
RL Neuron 19:371-379(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Vomeronasal neurons;
RA Ryba N.J.P., Tirindelli R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053990; AAC08417.1; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
FT NON TER 1
SQ SEQUENCE 230 AA; 25703 MW; 274BEP5P4D72F404 CRC64;

Query Match 45.5%; Score 904.5; DB 2; Length 230;
Best Local Similarity 76.6%; Pred. No. 4.1e-58;
Matches 177; Conservative 20; Mismatches 33; Indels 1; Gaps 1;

QY 138 NWSMAGQVTLALGFSLCLSGKTSSFLAYRISKSTQLTSMHPLYRKIIIVLSVLA 197
Db 1 NWTCMARQVTLALGFCLCLSSILGKTISLFFAYRISKSTRLISMHPIFRKLIVLCVVG 60

QY 198 EIGICTAYLILEPPMVYKNMESQNTKIILGCNEISIEFLYSMFGIDAFLLCFLTTFVA 257
Db 61 EIGVCTAYLMLKPPRMVKNIEPQNVKIIPECNEGSIEFLCSIPAPDVLLALLCFLTTFVA 120

QY 258 RQLPDNYYEGKCTIFGMLVFFIWMSPVYVLTSTGKFKMAVEIFAILASSHGLLGCI 317
Db 121 RKLPDNYYEGKCTIFGMLVFFIWMSPVYVLTSTGKFKMAVEIFAILASSYGLLGCI 180

QY 318 PKCLIIILRPNTSEIVCGRVSTTDNCIQLTSAFVSSELNNTTVSTVLDD 368
Db 181 PKCFIILRPKRNTDETGVGRVPTVDRSIQLASTSVSSEL-NTTVSTVLDE 230

RESULT 6
O93555 PRELIMINARY; PRT; 458 AA.
ID O93555
AC O93555;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative odorant receptor (Fragment).
GN Name=GF87;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RX MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;
RA Cao Y., Oh B.C., Stryer L.;
RT "Cloning and localization of two multigene receptor families in goldfish olfactory epithelium."
RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
DR EMBL; AF083084; AAC64079.1; --

DR	PRINTS; PRO0248; GPCRMR.	
DR	PRINTS; PRO1535; VOMERONASL2R.	
DR	PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.	
DR	PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.	
DR	PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.	
KW	Receptor.	
SQ	SEQUENCE 844 AA; 94598 MW; BOF13B4E7BAC4088 CRC64;	
Query Match 38.7%; Score 769.5; DB 2; Length 844;		
Best Local Similarity 41.8%; Pred. No. 9.9e-48;		
Matches 145; Conservative 72; Mismatches 129; Indels 1; Gaps 1;		
QY	2 PHSVCTDVCPPTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCCEGDEYWSNAQKSE 61	
DB	496 PRSACSESCPPGTRKAAQKGRPFCCYDCIPCAEGEISNETRFINCKPCPWEYWSNAEKNK 555	
QY	62 CVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVYVIHRHTPLVNASDWQLGFLIQVS 121	
DB	556 CVLKAVEFLSFTTEIMGVVLVFFSLFGVGLTLLVAILFYNNKDTPMVKANNSELSFLLIFS 615	
QY	122 LIIMLLSSMLFIDKPHNWSMAGQVTLALGFSCLSLGKTSSFLAYRISKSTQLTLS 181	
DB	616 LTLCLFCLSLTFIGRPTWESMCLCHTAFTGTFVLCISVLGKTIIVLMAFKATLPGNNIMK 675	
QY	182 -MHPLYRKIIIVLISVLAIEGICTAYLILEPDMVYKNMESQNTKIILGCNEISIEFLYSMF 240	
DB	676 WFGPAQQRSLVLAFTLIQVLIICVLWLTISPPFPYKMKYKKEIIECSLGSTIGFWAVL 735	
QY	241 GIDAFALALLCFLTTFVARQLPDNYVEGKCTIFGMLVFFIWMFSFVPVYLSTKGKFKMAVE 300	
DB	736 TYISLLAFCLFILAFARTLPDKFNEAKFTFSMLIFCAVWITFIPAYVSSPGKFTVAVE 795	
QY	301 IFAILASSHGLGCFAPKCLIIILLRPERNTSEIVCGRVSTTDCNIQ 347	
DB	796 IFAILSSSFGLLFGIFAPKCYIILLKPEQNTKQHLIGKTASVSLAQ 842	
RESULT 11		
O93556	PRELIMINARY; PRT; 350 AA.	
AC	O93556;	
DT	01-NOV-1998 (TReMBLrel. 08, Created)	
DT	01-NOV-1998 (TReMBLrel. 08, Last sequence update)	
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)	
DE	Putative odorant receptor (Fragment).	
GN	Name=GFE9;	
OS	Carassius auratus (Goldfish).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC	Cyprinidae; Carassius.	
OX	NCBI_TaxID=7957;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Olfactory epithelium;	
RX	MEDLINE=98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;	
RA	Cao Y., Oh B.C., Stryer L.;	
RT	"Cloning and localization of two multigene receptor families in goldfish olfactory epithelium.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).	
DR	EMBL; AF083085; AAC64080.1; --	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . . ; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	GO; GO:0007216; P:metabotropic glutamate receptor signaling p. . . ; IEA.	
DR	InterPro; IPR000337; GPCR_Mgr.	
DR	InterPro; IPR011500; NCD3G_GPCR.	
DR	InterPro; IPR004073; Vmron_receptor2.	
DR	Pfam; PF00003; 7tm_3; 1.	
DR	Pfam; PF07562; NCD3G; 1.	
DR	PRINTS; PR00248; GPCRMR.	
DR	PRINTS; PR01535; VOMERONASL2R.	
DR	PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.	
DR	PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.	
RESULT 12		
O73639	PRELIMINARY; PRT; 880 AA.	
AC	O73639;	
DT	01-AUG-1998 (TReMBLrel. 07, Created)	
DT	01-AUG-1998 (TReMBLrel. 07, Last sequence update)	
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)	
DE	Pheromone receptor.	
GN	Name=Cal3;	
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;	
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;	
OC	Tetraodontoidea; Tetraodontidae; Takifugu.	
OX	NCBI_TaxID=31033;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=98226788; PubMed=9560249; DOI=10.1073/pnas.95.9.5178;	
RA	Naito T., Saito Y., Yamamoto J., Nozaki Y., Tomura K., Hazama M.,	
RA	Nakanishi S., Brenner S.;	
RT	"Putative pheromone receptors related to the Ca2+-sensing receptor in Fugu.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).	
DR	EMBL; AB008861; BAA26126.1; --	
DR	HSSP; P23385; 1EWK.	
DR	GO; GO:0016020; C:membrane; IEA.	
DR	GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . . ; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	GO; GO:0007216; P:metabotropic glutamate receptor signaling p. . . ; IEA.	
DR	InterPro; IPR001828; ANF_receptor.	
DR	InterPro; IPR000337; GPCR_Mgr.	
DR	InterPro; IPR011500; NCD3G_GPCR.	
DR	InterPro; IPR004073; Vmron_receptor2.	
DR	Pfam; PF00003; 7tm_3; 1.	
DR	Pfam; PF01094; ANF_receptor; 1.	
DR	Pfam; PF07562; NCD3G; 1.	
DR	PRINTS; PR00248; GPCRMR.	
DR	PRINTS; PR01535; VOMERONASL2R.	
DR	PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.	
DR	PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.	
KW	Receptor.	
KW	Receptor.	

